

REPLACEMENT SHEET

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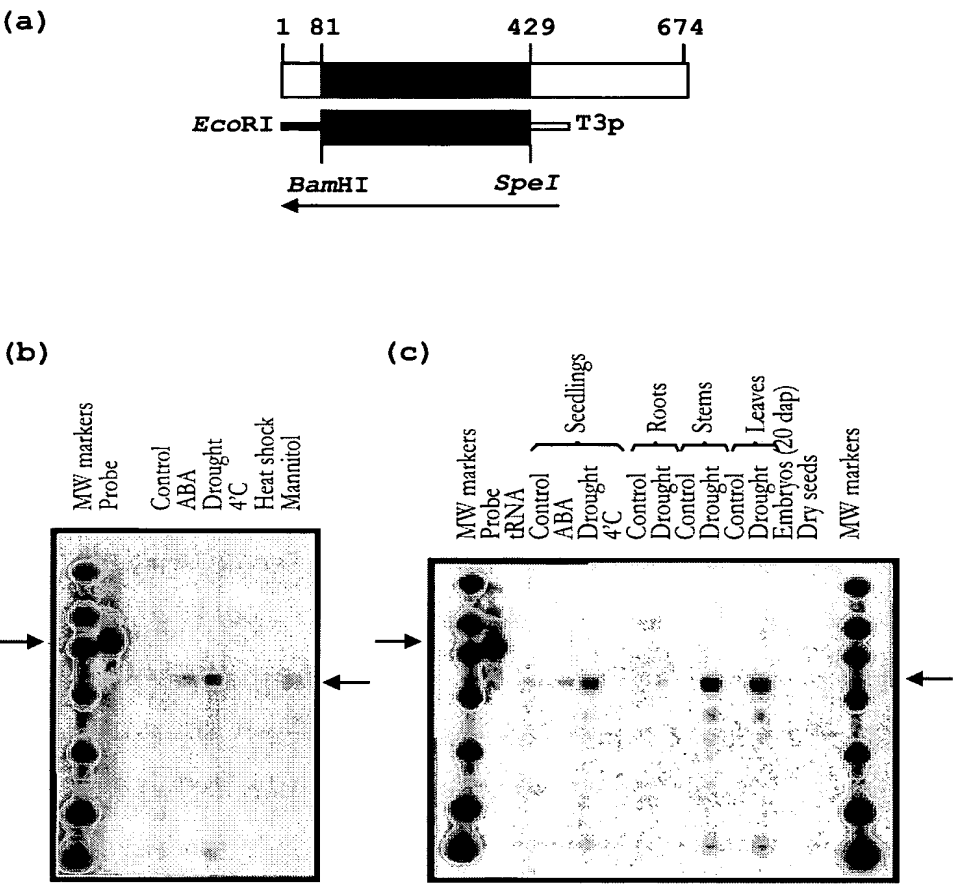
+1   TCACTAGTACCATAATATTTCACAAACACACACCTCAGAAACGAAGCTTGC
+53  ACATAATGTCTCTTCAACAAGTACCCACAACAGAAACAACCACCAGGAAGAA
1    M S L Q Q V P T T E T T T R K N
+105 CCGAAACGAGGGGCGGAAACGATTTACCGACAAACAAATAAGTTTCCTAGAG
17   R N E G R K R F T D K Q I S F L E
+157 TACATGTTTGAGACACAGTCGAGACCCGAGTTAAGGATGAAACACCAGTTGG
34   Y M F E T Q S R P E L R M K H Q L
+209 CACATAAACTCGGGCTTCATCCTCGTCAAGTGGCGATATGGTTCCAGAACAA
51   A H K L G L H P R Q V A I W F Q N K
+261 ACGCGCGCGATCAAAGTCGAGGCAGATTGAGCAAGAGTATAACGCGCTAAAG
69   R A R S K S R Q I E Q E Y N A L K
+313 CATAACTACGAGACGCTTGCGTCTAAATCCGAGTCTCTAAAGAAAGAGAATC
86   H N Y E T L A S K S E S L K K E N
+365 AGGCCCTACTCAATCAGgtatggttgcaaacttacaatgttgcatcaacta
103  Q A L L N Q
+417 ttttaagtagttttgaattttgtgacaataaagattgacaaatgttggtttga
+469 taattgattaacagTTGGAGGTGCTGAGAAATGTAGCAGAAAAGCATCAAGA
109   L E V L R N V A E K H Q E
+521 GAAAACTAGTAGTAGTGGCAGCGGTGAAGAATCGGATGATCGGTTTACGAAC
122   K T S S S G S G E E S D D R F T N
+573 TCTCCGGACGTTATGTTTGGTCAAGAAATGAATGTTCCGTTTGGCGACGGTT
139   S P D V M F G Q E M N V P F C D G
+625 TTGCGTACTTTGAAGAAGGAAACAGTTTGTGAGATTGAAGAACAACCTGCC
156   F A Y F E E G N S L L E I E E Q L P
+677 AGACCCTCAAAGTGGTGGGAGTTCTAAAGAGTAAAGAAGGATGTAGAAGTA
174   D P Q K W W E F *
+729 GTAGAGTAAAACTAAACATACCAGATAGTTGGTTTACACTTTGT
    
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Athb-1  LPEKKRRLTTEQVHLEKSFETENKLEPERKTOLAKKLGLQPRQVAVWFQNRARWTKQLERDYDLLKSTYDOLLSNYDSIVMDNKLIRSEVTSLTEK
Athb-6  LSEKKRRLSINQVKALEKNFLENKLEPERKVKLAQELGLQPRQVAVWFQNRARWTKQLEKDYGVLTQYDSLRNFDSIRRDNESLLQEISKLTKE
Athb-7  NKNNQRRFSDEQIKSLEMMFESETRLEPRKKVQLARELGLQPRQVAIWQNKRRARWKSQLETEYNILRQNYDNLASQFESLKKEKQALVSELQRLKEA
Athb-12 KSNNQRRFNEEQIKSLELIFESETRLEPRKKVQVARELGLQPRQMTIWFQNKRRARWTKQLEKEYNTRLRANYNNLASQFEIMKKEKQSLVSELQRLNEE
Hahb-4  RNEGRKRFTDKQISFLEYMFETQSRPELRMKHQLAHLGLHPRQVAIWQNKRRARSKSRQIEQYNAKKNYETLASKSESLLKENQALLNQLVLRNV
    
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FIG. 1

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FIG. 22

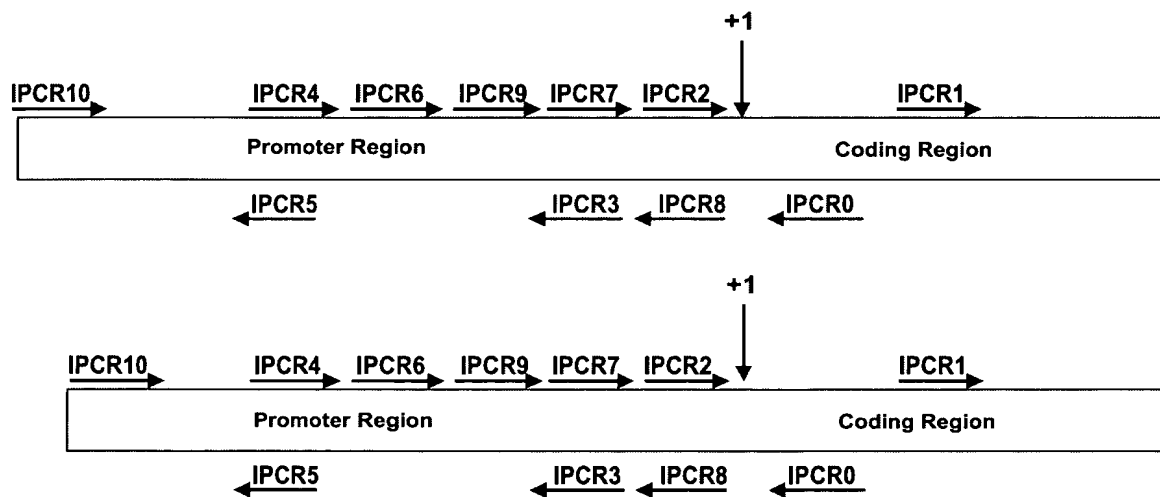


FIG. 23